

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:54:17 ; Search time 70 Seconds

(without alignments)
1087.611 Million cell updates/sec

Title: US-09-817-198C-2
Perfect score: 1105
Sequence: 1 MAKQYDVLFRLLIGDSGVG.....LBEKEGPGPANSSKTCWC 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues
Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
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 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdb*
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 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb*
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 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pdb*
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 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pdb*
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 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1105	100.0	212	9	US-09-817-198A-2
2	1105	100.0	212	15	US-10-363-616-319
3	1105	100.0	401	9	US-09-764-868-701
4	1092	98.8	218	9	US-09-817-198A-5
5	1077	97.5	212	9	US-09-817-198A-4
6	832	75.3	188	9	US-09-764-868-1120
7	573	51.9	208	16	US-10-408-765A-2929
8	559	50.6	224	14	US-10-369-493-4997
9	545	49.3	213	15	US-10-276-774-2286
10	540	48.9	221	15	US-10-264-049-2465
11	532	48.1	246	9	US-09-925-302-534
12	532	48.1	246	10	US-09-925-302-534
13	530.5	48.0	218	9	US-09-925-300-1571

14	528.5	47.8	207	9	US-09-794-257-8
15	528.5	47.8	207	14	US-10-170-385-373
16	528.5	47.8	207	14	US-10-400-991-65
17	526.5	47.6	200	16	US-10-408-765A-1301
18	523	47.3	206	14	US-10-128-714-8241
19	523	47.3	206	14	US-10-128-714-8600
20	518	46.9	214	17	US-10-425-115-357716
21	518	46.9	215	16	US-10-437-963-182164
22	518	46.9	251	15	US-10-425-114-65760
23	517	46.8	214	16	US-10-767-701-44111
24	514.5	46.6	215	16	US-10-437-963-115183
25	514	46.5	201	14	US-10-179-766-6
26	514	46.5	201	14	US-10-369-493-5076
27	514	46.5	214	17	US-10-425-115-204527
28	514	46.5	215	17	US-10-425-114-73047
29	513.5	46.5	215	17	US-10-425-115-361648
30	513.5	46.5	223	15	US-10-425-114-66036
31	513.5	46.5	248	15	US-10-437-963-182163
32	512.5	46.4	214	16	US-10-425-115-204526
33	512.5	46.4	215	17	US-10-425-115-204529
34	512.5	46.4	215	16	US-10-767-701-42756
35	512.5	46.4	216	15	US-10-425-114-65920
36	512.5	46.4	217	15	US-10-425-114-67764
37	512.5	46.4	217	15	US-10-425-114-70050
38	512.5	46.4	217	15	US-10-425-114-72771
39	512.5	46.4	217	15	US-09-822-860-5
40	512	46.3	190	9	US-09-817-198A-2
41	511.5	46.3	214	15	US-10-424-599-170355
42	511.5	46.3	214	16	US-10-767-701-42002
43	511.5	46.3	216	15	US-10-424-599-201556
44	511.5	46.3	218	17	US-10-425-115-224762
45	511	46.2	218	17	US-10-425-115-224759

ALIGNMENTS

RESULT 1

US-09-817-198A-2
; Sequence 2, Application US/09817198A
; Patent No. US20020146758A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001188
; CURRENT APPLICATION NUMBER: US/09/817,198A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Human
; US-09-817-198A-2

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Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIKVEVGKVRQ	60
Qy	61	IWDTAGERYQTITKYYRRAQGIIFLYVDISSRSYQHIMKWSVDVDEYAPGVQKILIG	120
Db	61	IWDTAGERYQTITKYYRRAQGIIFLYVDISSRSYQHIMKWSVDVDEYAPGVQKILIG	120
Qy	121	NKADEQKQVGRQGOOLAKYGMDFYTSACTNLNKSFTLTLVLQHRKELEGL	180
Db	121	NKADEQKQVGRQGOOLAKYGMDFYTSACTNLNKSFTLTLVLQHRKELEGL	180

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QY 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212
Db 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212

RESULT 2
US-10-363-616-319
; Sequence 319, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 319
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-319

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Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 60

QY 61 IWDTAGQERYQTITKQYRRAGIFLVYDISSERSYQHIMKWSDVDYAPGEGVKILIG 120
Db 61 IWDTAGQERYQTITKQYRRAGIFLVYDISSERSYQHIMKWSDVDYAPGEGVKILIG 120

QY 121 NKADBEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTRLTELVLQAHKLEGL 180
Db 121 NKADBEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTRLTELVLQAHKLEGL 180

QY 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212
Db 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212

RESULT 3
US-09-764-868-701
; Sequence 701, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 701
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-701

Query Match 100.0%; Score 1105; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 9.8e-100;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 60
Db 27 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 86

QY 61 IWDTAGQERYQTITKQYRRAGIFLVYDISSERSYQHIMKWSDVDYAPGEGVKILIG 120
Db 61 IWDTAGQERYQTITKQYRRAGIFLVYDISSERSYQHIMKWSDVDYAPGEGVKILIG 120

QY 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212
Db 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212

RESULT 4
US-09-817-198A-4
; Sequence 4, Application US/09817198A
; Patent No. US20020146758A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; FILE REFERENCE: CL001188
; CURRENT APPLICATION NUMBER: US/09/817,198A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-817-198A-4

Query Match 98.8%; Score 1092; DB 9; Length 218;
Best Local Similarity 97.2%; Pred. No. 8.1e-99;
Matches 212; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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Db 1 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 60

QY 61 IWDTAGQERYQTITKQYRRAGIFLVYDISSERSYQHIMKWSDVDYAPGEGVKILIG 120
Db 61 IWDTAGQERYQTITKQYRRAGIFLVYDISSERSYQHIMKWSDVDYAPGEGVKILIG 120

QY 121 NKADBEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTRLTELVLQAHK 174
Db 121 NKADBEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTRLTELVLQAHK 180

QY 175 KELEGLRMRASNELALAELEEEGKPEGPNSSKTCWC 212
Db 181 KELEGLRMRASNELALAELEEEGKPEGPNSSKTCWC 218

RESULT 5
US-09-817-198A-4
; Sequence 4, Application US/09817198A
; Patent No. US20020146758A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; FILE REFERENCE: CL001188
; CURRENT APPLICATION NUMBER: US/09/817,198A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-817-198A-4

QY 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212
Db 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212
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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:19:28 ; Search time 132 seconds
(without alignments)
106.511 Million cell updates/sec

Title: US-09-817-198C-2

Perfect score: 1105

Sequence: 1 MAKQYDVLFRLLIGDSGVG.....LEEEBKPEGPANGSKTCWC 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCBUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	527.5	47.7	205	2	US-08-531-525-25
4	527.5	47.7	205	2	US-08-718-270A-25
5	518.5	46.9	198	2	US-08-531-525-51
6	518.5	46.9	198	2	US-08-718-270A-51
7	515.5	46.7	203	4	US-09-255-920A-12
8	503.5	45.6	207	2	US-08-531-525-35
9	503.5	45.6	207	2	US-08-718-270A-35
10	494.5	44.8	215	2	US-08-531-525-10
11	494.5	44.8	215	2	US-08-718-270A-10
12	488.5	44.2	194	2	US-08-531-525-34
13	488.5	44.2	194	2	US-08-718-270A-34
14	478.5	43.3	201	2	US-08-916-901-3
15	478.5	43.3	201	3	US-09-154-602-3
16	473	42.8	213	4	US-09-248-796A-20293
17	469	42.4	201	2	US-08-916-901-8
18	469	42.4	201	3	US-09-154-602-8
19	467	42.3	205	4	US-09-709-103-49
20	467	42.3	205	4	US-09-439-410A-49
21	463	41.9	202	2	US-08-531-525-14
22	463	41.9	202	2	US-08-718-270A-14
23	462	41.8	227	4	US-09-248-796A-20291
24	453.5	41.0	201	2	US-08-531-525-13
25	453.5	41.0	201	2	US-08-718-270A-13
26	452.5	41.0	190	2	US-08-824-873-3
27	452.5	41.0	190	3	US-09-198-184-3

28	452.5	41.0	190	4	US-09-255-920A-7	Sequence 7, Appli
29	443	40.1	218	2	US-08-531-525-19	Sequence 19, Appl
30	443	40.1	218	2	US-08-718-270A-19	Sequence 19, Appl
31	438.5	39.7	227	4	US-09-270-767-46812	Sequence 46812, A
32	430.5	39.0	217	4	US-09-255-920A-15	Sequence 15, Appl
33	430	38.9	202	4	US-09-255-920A-11	Sequence 11, Appl
34	430	38.9	216	4	US-09-255-920A-14	Sequence 14, Appl
35	428	38.7	128	4	US-09-513-999C-5775	Sequence 5775, Ap
36	424	38.4	214	4	US-09-270-767-33012	Sequence 33012, A
37	424	38.4	214	4	US-09-270-767-48229	Sequence 48229, A
38	418	37.8	275	4	US-09-270-767-43635	Sequence 43635, A
39	416	37.6	191	3	US-09-075-454-3	Sequence 3, Appli
40	412.5	37.3	212	3	US-09-399-913-67	Sequence 67, Appl
41	412.5	37.3	212	4	US-09-350-614-67	Sequence 67, Appl
42	409.5	37.1	190	2	US-08-824-873-1	Sequence 1, Appli
43	409.5	37.1	190	3	US-09-198-184-1	Sequence 1, Appli
44	409.5	37.1	212	2	US-08-531-525-18	Sequence 18, Appl
45	409.5	37.1	212	2	US-08-718-270A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-824-873-4
; Sequence 4, Application US/08824873
; Patent No. 5843717
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl
; TITLE OF INVENTION: NOVEL RAB PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,873
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0240 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 234746
US-08-824-873-4

Query Match 49.3%; Score 545; DB 2; Length 207;
Best Local Similarity 52.9%; Pred. No. 3e-52;
Matches 99; Conservative 45; Mismatches 43; Indels 0; Gaps 0;

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 01:55:59 ; Search time 92 Seconds
(without alignments)
1325.863 Million cell updates/sec

Title: US-09-817-198c-2

Perfect score: 1105
Sequence: 1 MAKQYDVLFRLLIGDSGVG.....LBEERKPEGPANSKTCWC 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1105	100.0	212	RB15_HUMAN	P59190 homo sapien
2	1090	98.6	212	RB15_MOUSE	Q8k396 mus musculu
3	1077	97.5	212	RB15_RAT	P35289 rattus norv
4	872	78.9	212	Q6DI36	Q6di36 brachydanio
5	798	72.2	168	Q91YW0	Q91yw0 mus musculu
6	686	62.1	143	Q6P412	Q6p412 xenopus lae
7	686	62.1	143	AAH63736	AAH63736 xenopus l
8	533.5	51.0	200	Q7T384	Q7t384 brachydanio
9	557	50.4	211	Q7Y82	Q7y82 caenorhabdi
10	557	50.4	211	BAD07034	BAD07034 caenorhab
11	546.5	49.5	204	O15971	O15971 drosophila
12	545	49.3	207	RB8A_CANFA	P61007 canis famil
13	545	49.3	207	RB8A_HUMAN	P61006 homo sapien
14	545	49.3	207	AA335848	AA335848 homo sapi
15	541	49.0	207	Q8VCF6	Q8vcf6 m cell line
16	539.5	48.8	210	Q8VCF6	P22128 brachydanio
17	538.5	48.7	201	Q8DGVS	Q8dgvs drosopyge o
18	536	48.5	206	Q6DKL2	Q6dkl2 rattus norv
19	534.5	48.4	200	Q6PAW9	Q6paw9 xenopus lae
20	534.5	48.4	200	AAH60015	AAH60015 xenopus l
21	532	48.1	218	RB13_HUMAN	P61153 homo sapien
22	532	48.1	203	Q6GP66	Q6gp66 homo sapien
23	531.5	48.1	200	RB10_DISOM	P22127 discopyge o
24	530.5	48.0	200	RB10_CANFA	P24409 canis famil
25	530.5	48.0	200	RB10_HUMAN	P61026 homo sapien
26	530.5	48.0	200	RB10_MOUSE	P61027 mus musculu
27	530.5	48.0	200	CAG33584	CAG33584 homo sapi
28	528.5	47.8	203	RB13_RAT	P35286 rattus norv
29	528.5	47.8	207	RB8B_HUMAN	Q2930 homo sapien
30	528.5	47.8	207	RB8B_MOUSE	P61028 mus musculu
31	528.5	47.8	207	RB8B_RAT	P70550 rattus norv

32 528.5 47.8 207 2 O18338
33 528.5 47.8 207 2 BAD07038
34 526 47.6 202 1 RB13_MOUSE
35 526 47.6 206 1 RB8A_MOUSE
36 523.5 47.4 204 2 Q7QEG1
37 521 47.1 206 2 Q9HET4
38 520.5 47.1 299 2 Q7PUB2
39 519 47.0 216 2 O24466
40 518 46.9 205 2 Q7RVG3
41 518 46.9 214 2 Q40218
42 518 46.9 215 2 Q7XHP7
43 515.5 46.7 216 2 Q40215
44 515 46.6 216 2 Q6L502
45 515 46.6 216 2 Q9FJF1

O18338 drosophila
Bad07038 drosophil
Q9dd03 mus musculu
P52528 mus musculu
Q7qeg1 anopheles g
Q9het4 aspergillus
Q7pub2 anopheles g
O24466 arabidopsis
Q7rvg3 neurospora
Q40218 lotus japon
Q7xhp7 oryza sativ
Q40215 lotus japon
Q6L502 oryza sativ
Q9fjf1 arabidopsis

ALIGNMENTS

RESULT 1

RB15_HUMAN STANDARD; PRT; 212 AA.

AC P59190; Q86TX7; Q81W89;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ras-related protein Rab-15.

GN Name=RB15;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

IN [1]

SEQUENCE FROM N.A.

RX MEDLINE=22459283; PubMed=12508121; DOI=10.1038/nature01348;

RA Heilig R., Eckenberg R., Petit J.-L., Fonknechten N., Da Silva C.,

RA Catellio L., Levy M., Barbe V., De Berardinis V., Urte-Vidal A.,

RA Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S.,

RA Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C.,

RA Bruels T., Jaillon O., Friedlander L., Samson G., Brottier P.,

RA Cure S., Segrens B., Aniere F., Samain S., Crespeau H., Abbasi N.,

RA Alach N., Boscus D., Dickhoff R., Dors M., Dubois I., Friedman C.,

RA Gouvenoux M., James R., Madan A., Mailey-Estrada E., Mangenot S.,

RA Martins N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B.,

RA Vacherie B., Bellemere C., Belser C., Besnard-Gonnet M.,

RA Bartol-Mavel D., Boucard M., Briez-Silla S., Combette S.,

RA Dufosse-Laurent V., Ferron C., Lechaplais C., Louesse C., Muselet D.,

RA Magdelenat G., Pateau E., Petit E., Sirvain-Trukiewicz P., Trybou A.,

RA Vega-Czarny N., Bataille E., Bluet E., Bordelais I., Dubois M.,

RA Dumont C., Guerin T., Haffray S., Hammadi R., Muanga J., Fellouin V.,

RA Robert D., Wunderle E., Gauguet G., Roy A., Sainte-Marthe L.,

RA Verdier J., Verdier-Discala C., Hillier L.W., Fulton L., McPherson J.,

RA Matsuda F., Wilson R., Scarpelli C., Gyapay G., Wincker P., Saurin W.,

RA Quetier F., Waterston R., Hood L., Weissbach J., ;

RA Nature 421:601-607(2003).

RL Nature 421:601-607(2003).

RN Nature 421:601-607(2003).

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RK Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whitting N., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:09:38 ; Search time 78 Seconds
(without alignments)
261.512 Million cell updates/sec

Title: US-09-817-198c-2

Perfect score: 1105

Sequence: 1 MAKQYDVLFRLLIGDSGVG.....LLEEEKGPEGPANSSKTCWC 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1077	97.5	212	2 F42148	GTP-binding protei
2	559	50.6	224	2 T33855	hypothetical prote
3	545	49.3	207	2 B49647	GTP-binding protei
4	545	49.3	207	2 B36364	GTP-binding protei
5	532	48.1	203	2 A49647	GTP-binding protei
6	531.5	48.1	200	2 A38625	GTP-binding protei
7	530.5	48.0	200	2 D36364	GTP-binding protei
8	530	48.0	209	2 B38625	GTP-binding protei
9	526	47.6	206	2 I78851	GTP-binding protei
10	522.5	47.3	200	2 B42148	GTP-binding protei
11	519	47.0	216	2 T45901	GTP-binding protei
12	514	46.5	210	2 T28971	hypothetical prote
13	512	46.3	216	2 S33900	GTP-binding protei
14	512	46.3	216	2 T48378	GTP-binding protei
15	510	46.2	200	2 T12790	GTP-binding protei
16	509	46.1	215	2 T14565	GTP-binding protei
17	508.5	46.0	215	2 S57478	GTP-binding protei
18	508	46.0	216	2 J50640	GTP-binding protei
19	507.5	45.9	222	2 T14405	small GTP-binding
20	506	45.8	216	2 S57471	GTP-binding protei
21	505.5	45.7	217	2 S36365	GTP-binding protei
22	502.5	45.5	215	2 S57462	GTP-binding protei
23	501	45.3	203	2 S51495	GTP-binding protei
24	495.5	44.8	204	2 J57589	Sec4p homolog - ye
25	492.5	44.6	215	2 S57474	GTP-binding protei
26	483.5	43.8	208	2 A34716	GTP-binding protei
27	483	43.7	208	2 A38202	GTP-binding protei
28	482	43.6	203	2 S34253	GTP-binding protei
29	480	43.4	202	2 S38740	GTP-binding protei

RESULT 1

F42148

GTP-binding protein rab15 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: F42148

R:Elferink, L.A.; Anzai, K.; Scheller, R.H.

J. Biol. Chem. 267, 5768-5775, 1992

A:Title: rab15, a novel low molecular weight GTP-binding protein specifically expressed ;

A:Reference number: A42148; MUID:92210533; PMID:1313420

A:Accession: F42148

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-212 <RLF>

A:Cross-references: UNIPROT:P35289; GB:M83679; NID:G206536; PIDN:AAA1995.1; PID:G206537

A:Superfamily: ras transforming protein; translation elongation factor Tu homology

C:Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine

F:9-124/Domain: translation elongation factor Tu homology <ETU>

F:15-22/Region: nucleotide-binding motif A (P-loop)

F:121-124/Region: GTP-binding NKXD motif

F:210,212/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 97.5%; Score 1077; DB 2; Length 212;

Best Local Similarity 97.6%; Pred. No. 1e-78;

Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNBFHSHISTIGVDFFQMKTIEVDGIKVRIQ 60

Db 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNBFHSHISTIGVDFFQMKTIEVDGIKVRIQ 60

QY 61 IWDTAGQERYOTITKQYVRRAGIFLVYDIDISSERSYQHIMKWSDVDVAPGVQKILIG 120

Db 61 IWDTAGQERYOTITKQYVRRAGIFLVYDIDISSERSYQHIMKWSDVDVAPGVQKILIG 120

QY 121 NKADEQKQVREGQOQLAKEYGMDFYETSACTNLNIKESFRTLTELVLQAHKLEGL 180

Db 121 NKADEQKQVREGQOQLAKEYGMDFYETSACTNLNIKESFRTLTELVLQAHKLEGL 180

QY 181 RWRASNEALALEEEEGKPEGPANSSKTCWC 212

Db 181 RWRASNEALALEEEEGKPEGPANSSKTCWC 212

RESULT 2

T33855

hypothetical protein D1037.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-Jan-2000

C:Accession: T33855

R:Liedwith, J.; Biewald, T.

submitted to the EMBL Data Library, November 1998

A:Description: The sequence of C. elegans cosmid D1037.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 01:51:44 ; Search time 308 Seconds
(without alignments)
246.918 Million cell updates/sec

Title: US-09-817-198C-2

Perfect score: 1105

Sequence: 1 MAKQYDVLFRLLLLIGDSGVG.....LLEERGKPRGPNSSKTCWC 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1105	100.0	212	5	Abp62882 Human pol
2	1105	100.0	212	6	Aae29096 Human Ras
3	1105	100.0	401	4	Aau17136 Novel sig
4	1105	100.0	401	7	Adb93844 Human nov
5	1092	98.8	218	3	Aab41604 Human ORF
6	1077	97.5	212	7	Ades8127 Rat Prote
7	832	75.3	188	4	Aau17555 Novel sig
8	832	75.3	188	7	Adb94263 Human nov
9	573	51.9	208	7	Adj71123 Human hea
10	546.5	49.5	204	4	Abb70670 Drosophill
11	545	49.3	207	7	Ades8121 Human Pro
12	545	49.3	213	4	Abbi1916 Human ova
13	540	48.9	221	5	Abp41333 Human ova
14	532	48.1	203	7	Ades83429 Human Pro
15	532	48.1	203	7	Ades8125 Human Pro
16	532	48.1	246	3	Aab58196 Lung canc
17	530.5	48.0	200	3	Aab09979 Human aci
18	530.5	48.0	200	3	Aab19165 Amino aci
19	530.5	48.0	200	4	Aab95340 Human pro
20	530.5	48.0	200	8	Adn05082 Antipsori
21	530.5	48.0	218	3	Aab56993 Human pro
22	529.5	47.9	218	4	Abg07266 Novel hum
23	528.5	47.8	207	4	Abb71647 Drosophill
24	528.5	47.8	207	4	Aag67154 Amino aci
25	528.5	47.8	207	4	Aab92628 Human pro

26	528.5	47.8	207	5	ABP65204	Abp65204 Hypoxia-i
27	528.5	47.8	207	8	ADH68266	Adh68266 Human G-p
28	526.5	47.6	200	7	ADJ69495	Adj69495 Human hea
29	526	47.6	201	3	AA909982	AA909982 Canine Ra
30	523	47.3	199	3	AA909980	AA909980 Human Rab
31	523	47.3	199	3	AA909981	AA909981 Human Rab
32	523	47.3	206	6	ABJ26542	Abj26542 Aspergill
33	523	47.3	206	6	ABJ25583	Abj25583 Aspergill
34	519	47.0	216	3	AAG53945	Aag53945 Arabidops
35	519	47.0	216	3	AAG08688	Aag08688 Arabidops
36	519	47.0	253	3	AAG53944	Aag53944 Arabidops
37	519	47.0	254	3	AAG08687	Aag08687 Arabidops
38	514	46.5	201	6	AAO19956	AAO19956 C elegans
39	513.5	46.5	215	3	AAG35215	Aag35215 Zea mays
40	512	46.3	190	6	AAO26373	Aao26373 Ras-like
41	512	46.3	216	8	ADN72851	Adn72851 Thale cre
42	510	46.2	218	3	AAG19220	Aag19220 Arabidops
43	507	45.9	216	3	AAG08006	Aag08006 Arabidops
44	506.5	45.8	209	4	ABG23365	Abg23365 Novel hum
45	501	45.3	224	3	AAG47826	Aag47826 Arabidops

ALIGNMENTS

RESULT 1

ABP62882
ID ABP62882 standard; protein; 212 AA.

AC ABP62882;

DT 14-OCT-2002 (first entry)

DE Human polypeptide SEQ ID NO 319.

XX

Human; vulnary; dermatological; neuroprotective; nootropic; cancer;
antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
burn; central nervous system disorder; Alzheimer's disease;
Parkinson's disease; Huntington's disease; immune disorder;
autoimmune disorder; multiple sclerosis; diabetes; allergy.

OS Homo sapiens.

PN WO200218424-A2.

PD 07-MAR-2002.

PF 31-AUG-2001; 2001WO-US027093.

PR 01-SEP-2000; 2000US-00654935.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;

PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;

DR WPI; 2002-583321/62.

DR N-PSDB; ABQ93361.

New polynucleotide and polypeptides, useful for treatment and diagnosis
of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
sclerosis, diabetes and allergies.

PS Claim 20; SEQ ID NO 319; 284pp + Sequence Listing; English.

CC The invention relates to an isolated polynucleotide (I) comprising one of
245 sequences (ABQ93328-ABQ93532). Treating a condition comprising
administering to a mammalian subject a composition comprising the protein
(II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
(I), (II) and (III) are useful for diagnostic evaluation of disorders.
(I) is useful for gene therapy of diseases and (II) can be used for

CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 XX Sequence 212 AA;

Query Match 100.0%; Score 1105; DB 5; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2e-108;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 60
 Db 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 60
 QY 61 IWDTAGQERYQTITKQYRRAGGIFLVYDVISSESYQHIMKWSDVDEYAPGVQKILIG 120
 Db 61 IWDTAGQERYQTITKQYRRAGGIFLVYDVISSESYQHIMKWSDVDEYAPGVQKILIG 120
 QY 121 NKADDEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTLRLTELVLQAHKRELEGL 180
 Db 121 NKADDEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTLRLTELVLQAHKRELEGL 180
 QY 191 RMRASNELALAELEEEGKPEGPANSSKTCWC 212
 Db 191 RMRASNELALAELEEEGKPEGPANSSKTCWC 212

RESULT 2
 AA029096
 ID AA029096 standard; protein; 212 AA.

AC AA029096;

XX 24-FEB-2003 (first entry)

XX Human Ras-like protein.

XX Human; Ras-like protein; inflammation; cell proliferation; apoptosis;
 KW immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis;
 KW Parkinson's disease; wasting disease; cachexia; myocardial infarction;
 KW osteoporosis; atherosclerosis; glomerulonephritis; Crohn's disease;
 KW irritable bowel syndrome; multiple sclerosis; osteoarthritis; allergy;
 KW pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic;
 KW Sjogren's syndrome; infection; transgenic; gene therapy; neotropic; gout;
 KW neuroprotective; vasotropic; cytostatic; dermatological; nephrotropic;
 KW ophthalmological; tranquilizer; cancer; stroke; Grave's disease; AIDS;
 KW asthma; anaemia; drug screening.

XX Homo sapiens.

Key	Location/Qualifiers
Binding-site	15..22
Modified-site	/note= "ATP/GTP binding site motif A"
Modified-site	18..23
Modified-site	/note= "N-myristoylation site"
Modified-site	29..32
Modified-site	/note= "Casein kinase II phosphorylation site"
Modified-site	92..94
Modified-site	/note= "Protein kinase C phosphorylation site"
Modified-site	101..109
Modified-site	/note= "Tyrosine kinase phosphorylation site"
Modified-site	104..107
Modified-site	/note= "Casein kinase II phosphorylation site"
Modified-site	136..141
Modified-site	/note= "N-myristoylation site"
Modified-site	205..208
Modified-site	/note= "N-glycosylation site"
Modified-site	206..208

FT
 XX
 FN
 XX WO200277193-A2.
 PD
 XX 03-OCT-2002.
 XX
 XX 27-MAR-2002; 2002WO-US009328.
 XX
 XX 27-MAR-2001; 2001US-00817198.
 XX
 XX (PEKE) PE CORP.

XX Gan W, Ye J, Di Francesco V, Beasley EM;

XX WPI; 2003-018913/01.

XX N-PSDB; AAD47168, AAD47619.

XX New isolated human Ras-like protein polypeptide, useful for diagnosing,
 FT treating or preventing inflammation and disorders associated with cell
 FT proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma
 FT or stroke.
 XX
 XX Claim 1; Page 74; 82pp; English.

XX The invention relates to human Ras-like protein and its corresponding
 CC nucleic acid. The Ras-like protein and DNA is useful in the development
 CC of human therapeutics and diagnostic compositions. They are useful in the
 CC diagnosis, prevention and treatment of inflammation and disorders
 CC associated with cell proliferation and apoptosis, e.g. AIDS and other
 CC infectious or genetic immunodeficiencies, neurodegenerative disease e.g.
 CC Alzheimer's disease, Parkinson's disease, wasting diseases e.g. cachexia,
 CC ischaemic injuries e.g. myocardial infarction, stroke or reperfusion
 CC injury, toxin-induced diseases such as alcohol-induced liver damage or
 CC cirrhosis, osteoporosis or cancer. They are also used to treat disorders
 CC associated with inflammation including allergies, atopic dermatitis,
 CC atherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus,
 CC lupus erythematosus, multiple sclerosis, osteoarthritis, pancreatitis,
 CC autoimmune thyroiditis, rheumatoid arthritis, Sjogren's syndrome,
 CC helminthic infections. The antibodies of the invention are useful in
 CC pharmacogenomic analysis or for tissue typing. The transgenic animals are
 CC useful for studying the function of a Ras-like protein, and identifying
 CC and evaluating modulators of its activity. Ras-like protein is used in
 CC drug screening assays and its DNA is used in gene therapy. The present
 CC sequence is human Ras-like protein

XX Sequence 212 AA;

Query Match 100.0%; Score 1105; DB 5; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2e-108;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 60
 Db 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 60
 QY 61 IWDTAGQERYQTITKQYRRAGGIFLVYDVISSESYQHIMKWSDVDEYAPGVQKILIG 120
 Db 61 IWDTAGQERYQTITKQYRRAGGIFLVYDVISSESYQHIMKWSDVDEYAPGVQKILIG 120
 QY 121 NKADDEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTLRLTELVLQAHKRELEGL 180
 Db 121 NKADDEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTLRLTELVLQAHKRELEGL 180
 QY 181 RMRASNELALAELEEEGKPEGPANSSKTCWC 212
 Db 181 RMRASNELALAELEEEGKPEGPANSSKTCWC 212

XX RESULT 3

XX AAU17136

ID AAU17136 standard; protein; 401 AA.

ALIGNMENTS

```

US-09-817-198A-1
; Sequence 1, Application US/09817198A
; Patent No. US20020146758A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN
; TITLE OF INVENTION: NUCLEIC ACID MO
; TITLE OF INVENTION: PROTEINS, AND
; TITLE OF INVENTION: CU001188
; FILE REFERENCE: CU001188
; CURRENT APPLICATION NUMBER: US/09/8
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Versi
; SEQ ID NO 1
; LENGTH: 3257
; TYPE: DNA
; ORGANISM: Human
US-09-817-198A-1

```

Query Match	Score 3257;	DB 9;	Length 3257;
Best Local Similarity	100.0%;	Pred. No. 0;	
Mismatches 3257. Conservative	0;	Mismatches	0;
		Indels	0;
		Gaps	0;

1	TGCCCGCTGCCCGCCCGCGCAGTGTCCGGGCCCCCGCTGGCCCCAGTCAATGCGAAGCAGTACG	60
	QY	
	Db	
1	TGCCCGCTGCCCGCCCGCGCAGTGTCCGGGCCCCCGCTGGCCCCAGTCAATGCGAAGCAGTACG	60
	QY	
	Db	
61	ATGTGCTGTTCCGGCTGCTGCTGATCGGGGATCTCCGGGGTGGGCAAGACCTGCCTGCCTGT	120
	QY	
	Db	
61	ATGTGCTGTTCCGGCTGCTGCTGATCGGGGATCTCCGGGGTGGGCAAGACCTGCCTGCCTGT	120
	QY	
	Db	
121	GCCGCTTTCACGGACACGAGTTCACCTCTCGGCACATCTCCACCATCGGTGTGACTTTA	180
	QY	
	Db	
121	GCCGCTTTCACGGACACGAGTTCACCTCTCGGCACATCTCCACCATCGGTGTGACTTTA	180
	QY	
	Db	

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	3257	100.0	3257	9	US-09-817-198A-1		Sequence 1, Appli
2	2696.6	82.8	28770	9	US-09-817-198A-3		Sequence 3, Appli
3	1192.8	36.6	7924	15	US-10-311-455-2111		Sequence 2111, A
4	1192.8	36.6	7924	16	US-10-257-166-151		Sequence 151, Ap
5	1160.8	35.6	7924	15	US-10-311-455-2112		Sequence 2112, A
6	1160.8	35.6	7924	16	US-10-257-166-152		Sequence 152, Ap
7	1160.6	35.6	2021	9	US-09-764-868-88		Sequence 88, Appl
8	1000.2	30.7	1054	16	US-10-363-616-74		Sequence 74, Appl
9	599	18.4	601	9	US-09-817-198A-28		Sequence 28, Appl
10	599	18.4	601	9	US-09-817-198A-29		Sequence 29, Appl
11	569	17.5	594	15	US-10-029-386-7830		Sequence 7830, A
12	540	16.6	601	9	US-09-817-198A-30		Sequence 30, Appl

181 AGATGAAGACCATAGAGGTAGACGGCATCAAAAGTCGGGATACAGATCTGGGACACTGCAG 240
181 AGATGAAGACCATAGAGGTAGACGGCATCAAAAGTCGGGATACAGATCTGGGACACTGCAG 240
241 GGCAGGAGAGATACACAGACCATCACAAAGCAGTACTATCGGGGGCCAGAGGGGATATTTT 300
241 GGCAGGAGAGATACACAGACCATCACAAAGCAGTACTATCGGGGGCCAGAGGGGATATTTT 300
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361 TGGATGAGTACGACACAGAGCGCTTTACCGACATCATGAAAGTGGGTCAAGTGACG 420
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601 ATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGGCAAAACCCGAGGGCCACGCAACT 660
601 ATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGGCAAAACCCGAGGGCCACGCAACT 660
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 18:57:48 ; Search time 256 Seconds
(without alignments)
9043.123 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues
Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	202.6	6.2	412	4	US-09-513-999C-1698
2	174.2	5.3	730	4	US-09-300-958A-16
3	159.2	4.9	1799	4	US-09-774-528-36
4	156.6	4.8	1340	2	US-08-824-873-2
5	156.6	4.8	1340	3	US-09-198-184-2
6	156	4.8	925	2	US-08-916-901-4
7	156	4.8	925	3	US-09-154-602-4
8	145.2	4.5	615	4	US-09-513-999C-1782
9	144.6	4.4	3936	4	US-09-919-172-49
10	141	4.3	2552	4	US-09-270-767-12052
11	139	4.3	1053	4	US-09-255-990A-6
12	138	4.2	842	4	US-09-513-999C-2183
13	137	4.2	842	4	US-09-075-454-10
14	136.2	4.2	1106	3	US-09-620-312D-959
15	136.2	4.2	1106	4	US-09-484-970B-142
16	136.2	4.2	2612	4	US-09-620-312D-646
17	133.4	4.1	1069	4	US-09-620-312D-646
18	133	4.1	135	4	US-09-513-999C-16632
19	127.2	3.9	1090	4	US-09-799-451-914
20	124.2	3.8	723	4	US-09-016-434-1422
21	123.6	3.8	1102	4	US-09-620-312D-828
22	122.6	3.8	8137	4	US-09-566-921-7
23	120.6	3.7	847	2	US-08-773-423-4
24	119.6	3.7	684	4	US-09-248-796A-6188
25	118.4	3.6	928	4	US-09-270-767-14743
26	118	3.6	645	4	US-09-270-767-1383
27	118	3.6	645	4	US-09-270-767-16665

28	115.2	3.5	642	4	US-09-248-796A-6190	Sequence 6190, Ap	
29	115	3.5	833	4	US-09-620-312D-426	Sequence 426, App	
30	114.6	3.5	764	4	US-09-270-767-11701	Sequence 11701, A	
31	113	3.5	639	3	US-09-399-913-66	Sequence 66, Appl	
32	113	3.5	639	4	US-09-350-614-66	Sequence 66, Appl	
33	110	3.4	970	3	US-08-888-077A-28	Sequence 28, Appl	
34	106.2	3.3	1054	4	US-09-976-594-1096	Sequence 1096, Ap	
35	104.2	3.2	1308	4	US-09-270-767-12890	Sequence 12890, A	
36	102.2	3.1	3745	4	US-09-976-594-387	Sequence 387, App	
37	101.4	3.1	408	4	US-09-270-767-27320	Sequence 27320, A	
38	98.8	3.0	404	4	US-09-513-999C-2692	Sequence 2692, Ap	
39	96.4	3.0	254	4	US-09-513-999C-32591	Sequence 32591, A	
c	40	93.8	2.9	193	4	US-09-702-705-989	Sequence 989, App
c	41	93.8	2.9	193	4	US-09-702-705-1161	Sequence 1161, App
c	42	93.8	2.9	193	4	US-09-736-457-989	Sequence 989, App
c	43	93.8	2.9	193	4	US-09-736-457-1161	Sequence 1161, App
c	44	93.8	2.9	193	4	US-09-614-124B-989	Sequence 989, App
c	45	93.8	2.9	193	4	US-09-614-124B-1161	Sequence 1161, App

ALIGNMENTS

RESULT 1
US-09-513-999C-1698
; Sequence 1698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1698
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29...412
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 385
; OTHER INFORMATION: y=c or t
US-09-513-999C-1698

Query Match 6.2%; Score 202.6; DB 4; Length 412;
Best Local Similarity 68.1%; Pred. No. 3e-45;
Matches 280; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

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DB	1	GCATTCCCGTCGGGGAGAGAGTGAATATGCGAAGACCTACGATTACCTGTCAAGCT 60
QY	77	GCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCTGCTGCTGCTTCCACGACAA 136
DB	61	GCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCTGCTGCTTCCGCTTCTCCGAGGA 120
QY	137	CGAGTTCCCACTCTCCGACATCTCCACCATCGGTGTTGACTTTAAGATGAAGACCATAGA 196
DB	121	CGCTTCAACTCCACCTTTTATCTCCACCATAGAAATGACTTTAAATTTAGGACCATAGA 180
QY	197	GGTAGACGGCATCAAAAGTCGGGATACAGATCTGGGACACTGCGAGGCGAGGAGATACCA 256
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QY 257 GACCATCAAAAGCAGTACTATCGCGCGCCAGGGGATATTTTGGTCTATGACATTAG 316
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361 TCGAGACGTCGAAAAGATGATACTYGGGAACAAGTGTGATGTGAATGCAA 411

RESULT 2

US-09-300-958A-16
; Sequence 16, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: Using Same
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 730
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-16

Query Match 5.3%; Score 174.2; DB 4; Length 730;
Best Local Similarity 56.7%; Pred. No. 2.5e-37;
Matches 342; Conservative 0; Mismatches 258; Indels 3; Gaps 1;

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QY 67 TGTTCGGCTGCTGCTGATCGGGACTCCGGGTGGGCAAGACTGCTGCTGTCGCGCT 126
Db 104 TCTTCAAGCTGCTCATCATCGCGACAGCGGTGTGGGCAAGAGCAGTTTACTTTGCGTT 163
QY 127 TCACCGACAAACGAGTTCCACTCTCGCACATCTCCACCATCGGTGTTGACTTTAAGATGA 186
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QY 187 AGACCATAGAGTAGAGCGCATCAAGTGGGATACAGATCTGGGACACTCGAGGGCAGG 246
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QY 367 AGTACCCAGAGCGGTCCAGAGATCTTATTGGGAATAGGCTGATGAGGAGCAGA 426
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QY 427 AACGGCAGGTGGGAAGAGAGCAAGGCGCAGCTGCGGAGGAGTATGCGATGGACTTCT 486

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QY 607 TGG 609
Db 641 TGG 643

RESULT 3

US-09-774-528-36
; Sequence 36, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 36
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(831)
US-09-774-528-36

Query Match 4.9%; Score 159.2; DB 4; Length 1799;
Best Local Similarity 59.5%; Pred. No. 5.4e-33;
Matches 288; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

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Db 383 GGGACACAGCAGGTCCAGAGAGATTCAACAGCATTTACTCAGCTTATTACAGAGTGCCA 442
QY 289 AGGGGATATTTTGGTCTATGACATTAGCAGCGAGCGCTTTTACCAGACATCATGAGT 348

GenCore version 5.1.6
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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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13	797.2	24.5	840	5	BQ557215 AGENCOURT
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16	781.2	24.0	1027	4	BM476862 AGENCOURT
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24	743.6	22.8	793	6	CA411919 UI-H-E20-

25	742	22.8	756	5	BX093757	BX093757 BX093757
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27	723.6	22.2	730	5	BX331206	BX331206 BX331206
28	722	22.2	732	4	EM045331	EM045331 603623321
29	721.8	22.2	749	4	BG769088	BG769088 602743340
30	716.8	22.0	766	4	EM049329	EM049329 603628279
31	709	21.8	748	7	CN352234	CN352234 170005315
32	704.6	21.6	724	5	BX352668	BX352668 BX352668
33	704.6	21.6	731	5	BX388608	BX388608 BX388608
34	698.2	21.4	1116	5	BQ067682	BQ067682 AGENCOURT
35	697	21.4	744	4	BG697415	BG697415 UI-CF-EC1
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38	689.4	21.2	883	4	BG766350	BG766350 602739059
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43	644.2	19.8	891	2	BE883791	BE883791 601506187
44	638	19.6	639	5	BQ188717	BQ188717 UI-E-EJ1-
45	632.2	19.4	637	6	CA424721	CA424721 UI-H-FB1-

ALIGNMENTS

RESULT 1
CNSLTI18T 3151 bp mRNA linear HTC 18-JUN-2003
LOCUS human full-length cDNA clone CS0DI028YML1 of Placenta of Homo sapiens (human).
DEFINITION
ACCESSION BX248046
VERSION BX248046.1 GI:28193221
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3151)
Li W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 3151)
Genoscope.
Direct Submission
Submitted (30-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
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LVVDISERSYQHIMKWVSDVDEVDATSLPGCGASPGKARRGDPGKANSRKLCL
POPMKTSQTHQASRRSLIGRLMRSRNGRWEESKSSGSSRRSMAWTSMKQVPAPTST
LKSHSRV"

ORIGIN

Query Match 88.2%; Score 2874.2; DB 3; Length 3151;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 3; Indels 131; Gaps 1;

QY 168 GGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAAGTCGGATACAGATC 227
DB 1 GGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAAGTCGGATACAGATC 60

QY 228 TGGGACACTGACAGGACGAGAGATACACAGACCATCAAAAGCAGTACTATCGCGGGGCC 287
DB 61 TGGGACACTGACAGGACGAGAGATACACAGACCATCAAAAGCAGTACTATCGCGGGGCC 120

QY 288 CAGGGGATATTTTGGTCTATGACATTAAGCAGGAGCGCTCTTACAGCACATCATGAAG 347
DB 121 CAGGGGATATTTTGGTCTATGACATTAAGCAGGAGCGCTCTTACAGCACATCATGAAG 180

QY 348 TGGGTCAGTGACGTGGATGA----- 367
DB 181 TGGGTCAGTGACGTGGATGAGGTAGGATGCCACCTCACTGCCGGGGTGTGGAGAGGGT 240

QY 368 ----- 367
DB 241 GCCTCACCGGGGAGGCAAGGCGAGGGCCAGATGGGAAGGCAATGCTTCCAGGAAGCTT 300

QY 368 -----GTAGGCACAGAAAGGGGTCTCAGAGATCC 396
DB 301 TGCCTTCCACAGCCCTGGATGAAGACCTCTGGTACGCCACCAAGAGGGGTCCAGAAGATCC 360

QY 397 TTATTTGGGAATAAGGCTGATGAGGAGCAGAAACCGCAGGTGGGAAGAGAGCAAGGGCAGC 456
DB 361 TTATTTGGGAATAAGGCTGATGAGGAGCAGAAACCGCAGGTGGGAAGAGAGCAAGGGCAGC 420

QY 457 AGCTGGGGAAGGAGTATGGCATGACCTTATGAAACAAAGTGCCTGCACCAACCTCAACA 516
DB 421 AGCTGGGGAAGGAGTATGGCATGACCTTATGAAACAAAGTGCCTGCACCAACCTCAACA 480

QY 517 TTAAGAGTCAATTCACGCTCTGACAGAGCTGGTGTGCGAGGCCCATAGGAAGAGCTGG 576
DB 481 TTAAGAGTCAATTCACGCTCTGACAGAGCTGGTGTGCGAGGCCCATAGGAAGAGCTGG 540

QY 577 AAGCCCTCCGATGCGTCGACGAATAGTTGGCACTTGGCAGAGCTGGAGGAGGAGG 636
DB 541 AAGCCCTCCGATGCGTCGACGAATAGTTGGCACTTGGCAGAGCTGGAGGAGGAGG 600

QY 637 GCAAAACCGAGGGCCAGCGAATCTTCGAAACCTGCTGGTCTGAGTCTGTGTGGGG 696
DB 601 GCAAAACCGAGGGCCAGCGAATCTTCGAAACCTGCTGGTCTGAGTCTGTGTGGGG 660

QY 697 CACCCACACGACACCCCTCTTCCCTCAGGAGGCCGTGGGACAGACAGGGAGCCGGGC 756
DB 661 CACCCACACGACACCCCTCTTCCCTCAGGAGGCCGTGGGACAGAGGGAGCCGGGC 720

QY 757 TTTGCCCTGCTGCTCTCTGTGTGATGAACCTATGATGATACAGTACCACTACTCC 816
DB 721 TTTGCCCTGCTGCTCTCTGTGTGATGAACCTATGATGATACAGTACCACTACTCC 780

QY 817 CCCTGCTGSCCTGAGAGGGCTCTGCTGATCTCAAGCAGCCCTGTCCCGAGCCCG 876
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QY 877 TCACCCCTGGAGTGTCTTCTTCAGGCTGTTCCTCCAGCCACAGGCGCTCTACGACCCCC 936
DB 841 TCACCCCTGGAGTGTCTTCTTCAGGCTGTTCCTCCAGCCACAGGCGCTCTACGACCCCC 900

QY 937 ACGATGCGCGAGACATGCTCACCATCCCGACCCACAGACAAAGCAGGCGGTGG 996
DB 901 ACGATGCGCGAGACATGCTCACCATCCCGACCCACAGACAAAGCAGGCGGTGG 960

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DB 1021 TCTCTTCCCCCACTTCTCTTCTCTGACCCCTCCCTCCGGTGGTTCGTATCAAGCT 1080

QY 1117 CTTCAAAACCCCGTCCCGGTGTCTGTGTGTGAGCTCGCTCTTCTCTCTCTCTCTA 1176
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QY 1177 AGCTATCCAAAGGGATGGACCCAGGCTCGTGGGAGGTTCCACCCCTGGATCCAGAGA 1236
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QY 1237 ACCCTCACCCCTCGTGGGTGGCCAAAGGCTACAGGGTCTTCTTCTCTCTCTCTCT 1296
DB 1201 ACCCTCACCCCTCGTGGGTGGCCAAAGGCTACAGGGTCTTCTTCTCTCTCTCTCT 1260

QY 1297 ACCCCCACTGTCTCTCATGTGCCATGGGCTGTCTCCCAAGTGAAGTGGAGC 1356
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QY 1357 ATCGAGGTAGGAGGGAAACAGCAACCGGGAGTCTCTCGAGCCTGGGGCTGCCCTACTCT 1416
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QY 1417 ACCCATTCGCCCAACAGAGCTTTTGGCTTGGCTGGCCGCCCTCTTTTGGGGAAC 1476
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QY 1477 TGAAGCTCAGAGCAGGTCCTTCAAGAGGAAACAAATGAGGGGTGGCAGGATAAAAA 1536
DB 1441 TGAAGCTCAGAGCAGGTCCTTCAAGAGGAAACAAATGAGGGGTGGCAGGATAAAAA 1500

QY 1537 GTCACTCTCATTTCTTACCTCCCATGCAATGAAACAAATTTCTCTCCACCTGCTCC 1596
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QY 1597 AAATTTAAAGATGTGGAACAAAGCCTGTGGTACTTCCAGGGGCAAGAGAGCCCTGGGT 1656
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QY 1657 CAGTCACACTGTCAAGCCCAACATGCACTCCACAAAGGGGAGCATTTTGGAAATGAGGAC 1716
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QY 1717 TAGCTCTATGTATCAGGTTAAGAGCAAGGAGAGCTGGCCAGGACAGAGATTTGCACA 1776
DB 1681 TAGCTCTATGTATCAGGTTAAGAGCAAGGAGAGCTGGCCAGGACAGAGATTTGCACA 1740

QY 1777 GCAGAGGGGAATGTAGCAACAGCAGGGGCTCTTAGGCCCATCTTTCATTTCTTAGGTAA 1836
DB 1741 GCAGAGGGGAATGTAGCAACAGCAGGGGCTCTTAGGCCCATCTTTCATTTCTTAGGTAA 1800

QY 1837 GAAGAGCATTTCTCAGACTCCAGGGGAGGAGCTGAGCCCTAGCCTTTCAGCAACCAAGGT 1896
DB 1801 GAAGAGCATTTCTCAGACTCCAGGGGAGGAGCTGAGCCCTAGCCTTTCAGCAACCAAGGT 1860

QY 1897 TCTCTGGGACCCCAAGTTTATGGGAGAGGGGCAAGACTTTCATGGGAAGAGAGAGAA 1956
DB 1861 TCTCTGGGACCCCAAGTTTATGGGAGAGGGGCAAGACTTTCATGGGAAGAGAGAGAA 1920

QY 1957 GGCCCTGGGTAGAAACCGTTGGTCTGTCTCTTTGGGCTTTAAGACAAAGCGCTCATCT 2016
DB 1921 GGCCCTGGGTAGAAACCGTTGGTCTGTCTCTTTGGGCTTTAAGACAAAGCGCTCATCT 1980

QY 2017 TGCCCTCTACTCTCTGATAGGCTTTGGCGTTTGGCAACCACTGTGGCTACAGGTGGAG 2076
DB 1981 TGCCCTCTACTCTCTGATAGGCTTTGGCGTTTGGCAACCACTGTGGCTACAGGTGGAG 2040

QY 2077 GGAAGGAGACTCTTCTCTCAGAGTGTATGTTTCAGGAAGTTTCTTTTAAACCCCATATGGC 2136
DB 2041 GGAAGGAGACTCTTCTCTCAGAGTGTATGTTTCAGGAAGTTTCTTTTAAACCCCATATGGC 2100

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 18:56:50 ; Search time 13354 Seconds
(without alignments)
11533.814 Million cell updates/sec

Title: US-09-817-198C-1

Perfect score: 3257
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Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_hq:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_to:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3030.2	93.0	3326	9 BC040679	BC040679 Homo sapi
2	2696.6	82.8	190517	9 AL139022	AL139022 Human chr
3	1423.8	43.7	2210	9 HSM806937	EX640825 Homo sapi
4	1192.8	36.6	7924	6 AX347040	AX347040 Sequence
5	1192.8	36.6	7924	6 AX348456	AX348456 Sequence
c 6	1160.8	35.6	7924	6 AX347041	AX347041 Sequence
c 7	1160.8	35.6	7924	6 AX348457	AX348457 Sequence
8	1000.2	30.7	1054	6 AX399903	AX399903 Sequence
9	866.2	26.6	895	6 BD205055	BD205055 Human nuc
10	866.2	26.6	895	6 AX014147	AX014147 Sequence
11	813	25.0	3139	10 BC027769	BC027769 Mus muscu
12	633	19.4	676	6 AX781147	AX781147 Sequence
13	577.6	17.7	945	10 RATRAB15X	M03679 Sprague-Daw
14	496	15.2	579	6 CO730386	CO730386 Sequence
15	477.4	14.7	481	6 AX396088	AX396088 Sequence
c 16	438.8	13.5	463	6 AX334820	AX334820 Sequence
17	423.6	13.0	270654	2 AC096084	AC096084 Rattus no
18	416.4	12.8	2560	10 BC013790	BC013790 Mus muscu
19	383	11.8	410	6 AX779778	AX779778 Sequence

20	378.4	11.6	176940	10 AC132331	AC132331 Mus muscu
21	378.2	11.6	1980	5 BC075754	BC075754 Danio rer
22	338.2	10.4	2348	5 BC063736	BC063736 Xenopus l
23	307	9.4	313	6 AX341683	AX341683 Sequence
24	234.2	7.2	2048	9 BC002977	BC002977 Homo sapi
25	234.2	7.2	2818	9 AK025165	AK025165 Homo sapi
26	230.6	7.1	624	9 CR536583	CR536583 Homo sapi
27	230.6	7.1	1980	9 SS3268	SS3268 Homo sapien
28	229	7.0	621	9 CR542274	CR542274 Homo sapi
29	229	7.0	624	9 AF498943	AF498943 Homo sapi
30	229	7.0	624	9 BT007184	BT007184 Homo sapi
31	229	7.0	624	12 BT008275	BT008275 Synthetic
32	229	7.0	660	9 HSMRAB8	X56741 H.sapiens m
33	229	7.0	1971	6 CQ726143	CQ726143 Sequence
34	227.4	7.0	638	10 SS3270	SS3270 MBL=RAS-rel
35	225.4	6.9	1400	10 BC071176	BC071176 Rattus no
36	224.2	6.9	1337	10 BC019990	BC019990 Mus muscu
37	222.6	6.8	760	4 CFRAB8	X56385 Canine rab8
38	222	6.8	1018	5 BX930100	BX930100 Gallus ga
39	221.4	6.8	563	5 BX934711	BX934711 Gallus ga
40	218.2	6.7	765	5 DYGORA2	M38391 Discopyge o
41	217.8	6.7	624	6 AX236078	AX236078 Sequence
42	217.8	6.7	1128	9 BC020654	BC020654 Homo sapi
43	217.8	6.7	1161	6 AX236076	AX236076 Sequence
44	217.8	6.7	1265	9 AB038995	AB038995 Homo sapi
45	217.8	6.7	1266	6 CQ725816	CQ725816 Sequence

ALIGNMENTS

BC040679 3326 bp mRNA linear PRI 29-JUN-2004
Homo sapiens RAB15, member RAS oncogene family, mRNA (cDNA clone MGC:42319 IMAGE:4817835), complete cds.

ACCESSION BC040679

VERSION MGC

KEYWORDS MGC

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 3326)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butler, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL 12477932

PUBMED 2 (bases 1 to 3326)

REFERENCE Strausberg, R.

AUTHORS Direct Submission

TITLE Submitted (29-NOV-2002) National Institutes of Health, Mammalian

JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Sep 16, 2003 this sequence version replaced gi:26251822.
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Pession, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palquist, Anca Petrescu, Anna Lilisa Prambu,
Parvaneh Saeedi, JR Santos, Angeliqwe Schnerch, Ursula Skaleka,
Duane Smalish, Jeff Scott, Miranda Tsai, George Yang, Jacqueline
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 70 Row: p Column: 2.

QY	341	CATGAAGTGGGTCACTGACGTCGATGA-----	367
Db	301	CATGAAGTGGGTCACTGACGTCGATGAGTGGATGCCACTCACTGCCGGGGTGTGG	360
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Db	361	AGAGGGTGCTCACCGGGGAGGCCAAGCGGAGGGCCAGATGGGAAGGCCAAATGCCTTCCAG	420
QY	368	-----GTACGCCACCAAGAGCGCTCCAG	389
Db	421	GAAGCTTTTGGCTTCCACAGCCCTCGATGAAGACCTCTGTGTACGCCACCAAGAGCGCTCCAG	480
QY	390	AGATGCTCTATTGGGAATAAGCTCTATCAGGAGCAGAAACCGCAGCTGGGAAAGAGCAA	449
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Db	541	GGGCAGCAGCTGGCGAAGGATATGGCATGGACTTCTATGAAACAAGTGCCCTGCACCAAC	600
QY	510	CTCAACATTAAAGATCATTCACGGCTCTGACAGAGCTGGTGTCTGCAGGCCCATAGGAAG	569
Db	601	CTCAACATTAAAGATCATTCACGGCTCTGACAGAGCTGGTGTCTGCAGGCCCATAGGAAG	660
QY	570	GAGCTTGAAGGCTCCGATGCTGCCAGCAATGAGTTGGCACTGGCAGAGCTGGAGAG	629
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QY	630	GAGAGGGCAAAACCGAGGGCCACAGCGAACTCTTCGAAACCTGTGTGTCTGATCTGT	689
Db	721	GAGAGGGCAAAACCGAGGGCCACAGCGAACTCTTCGAAACCTGTGTGTCTGATCTGT	780
QY	690	TGTGGGGCACCACACAGACACCCCTCTTCCCTCAGGAGGCCCTGTGGCAGACAGGGGAG	749
Db	781	TGTGGGGCACCACACAGACACCCCTCTTCCCTCAGGAGGCCCTGTGGCAGACAGGGGAG	840
QY	750	CCGGGGCTTTGCCCTGTCTGTCTCTCTGTGTGATGATCAACCTATTGAGTATACGTAGCCA	809
Db	841	CCGGGGCTTTGCCCTGTCTGTCTCTCTGTGTGATGATCAACCTATTGAGTATACGTAGCCA	900
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QY	870	CAGCCCTGCACCTGGAGTGGTCTTCTTCTCAGCCTGTTTCCACAGCCACAGGCCCTGTCTAC	929
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QY	930	GACCCCAAGATGTCCGCAAGCACTGTCTCAACATCCGACCCACCCACAGCAACAGCCA	989
Db	1021	GACCCCAAGATGTCCGCAAGCACTGTCTCAGCATCCCGCACCCACAGCAACAGCCA	1080
QY	990	GGGCTGAGTCCAGGCCACTTTCAGCTGTCTCTTCTCCGTCGATCGTGTCTTCTCTG	1049
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QY	1050	CTTTTCTCTCTTCCCCACTTCTTCTTCTGACCCCTCCCTCCGGTGCCTTCTGAT	1109
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QY	1170	CTTCTCTAAGTATCCAAAGGGGATGGACCAAGGCTCGTGGGAGTTCCACCCCTTGGATCC	1229
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